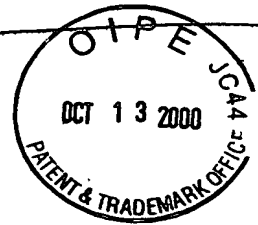


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<213> *Saccharomyces cerevisiae*

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Thr Ala Leu Val Thr Ala Ala Gly Thr His Arg Asn Ser Ser Thr Ala
      35              40              45

```

```

Lys Thr Val Glu Thr Glu Asp Gly Glu Glu Asp Ile Asp Glu Tyr Gln
      50              55              60

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Arg Lys Arg Ala Ala Gly Ser Gly Glu Ser Thr Pro Glu Arg Ser Asp
      65              70              75              80

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Phe Lys Arg Val Lys His Asp Asn His Lys Thr Leu His Pro Val Asn
      85              90              95

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Leu Gln Asn Thr Gly Ala Ala Ser Val Asp Asn Asp Gly Leu His Asn
      100             105             110

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Leu Thr Asp Ile Ser Asn Asp Ala Glu Lys Leu Leu Met Ser Val Asp
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Asp Gly Ser Ala Ala Pro Ser Thr Leu Ser Val Asn Met Gly Val Ala
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Ser His Asn Val Ala Ala Pro Thr Thr Val Asn Ala Ala Thr Ile Thr
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Gly Ser Asp Val Ser Asn Asn Val Asn Ser Ala Thr Ile Asn Asn Pro
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Met Glu Glu Gly Ala Leu Pro Leu Ser Pro Thr Ala Ser Ser Pro Gly
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 Ala Tyr Phe Lys Asn Leu Leu Phe Arg Leu Val Ala Asn Met Asp Arg
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 Ser Glu Leu Ser Asp Leu Gly Thr Leu Ile Lys Asp Asn Leu Lys Arg
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 Asp Leu Ile Thr Ser Leu Pro Phe Glu Ile Ser Leu Lys Ile Phe Asn
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 Trp Asn Lys Ile Ile Arg Lys Ser Thr Ser Leu Trp Lys Lys Leu Leu
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 Val Thr Gly Ser Arg Asp Asn Thr Leu His Val Trp Lys Leu Pro Lys
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 Lys Cys Leu Tyr Ile Leu Ser Gly His Thr Asp Arg Ile Tyr Ser Thr
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 Ser Tyr Ala Thr Asn Ser Ala Ser Pro Cys Ala Lys Ile Leu Gly Ala
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 Ser Asp Lys Phe Leu Val Ser Ala Ala Ala Asp Gly Ser Ile Arg Gly
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<213> Homo sapiens

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Arg Leu Cys Leu Asn Gln Glu Thr Val Cys Leu Ala Ser Thr Ala Met
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1
ant

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 Glu Lys Glu Leu Cys Val Lys Tyr Phe Glu Gln Trp Ser Glu Ser Asp
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<210> 8

<211> 640

<212> PRT

<213> *Saccharomyces cerevisiae*a1
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 50 55 60
 Thr Arg Ser Pro Ser Ser Ser Pro Asp Leu Ala Thr Asn Asp Ser Gly
 65 70 75 80
 Thr Arg Val Gln Pro Leu Pro Glu Tyr Asn Phe Thr Lys Phe Cys Tyr
 85 90 95
 Arg His Asn Pro Asp Ile Gln Phe Ser Pro Thr His Thr Ala Cys Tyr
 100 105 110
 Lys Gln Asp Leu Lys Arg Thr Gln Glu Ile Asn Ala Asn Ile Ala Lys
 115 120 125
 Leu Pro Leu Gln Glu Gln Ser Asp Ile His His Ile Ile Ser Lys Tyr
 130 135 140
 Ser Asn Ser Asn Asp Lys Ile Arg Lys Leu Ile Leu Asp Gly Ile Leu
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 Ser Thr Ser Cys Phe Pro Gln Leu Ser Tyr Ile Ser Ser Leu Val Thr
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 His Met Ile Lys Ile Asp Phe Ile Ser Ile Leu Pro Gln Glu Leu Ser
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 Leu Lys Ile Leu Ser Tyr Leu Asp Cys Gln Ser Leu Cys Asn Ala Thr
 195 200 205
 Arg Val Cys Arg Lys Trp Gln Lys Leu Ala Asp Asp Asp Arg Val Trp
 210 215 220
 Tyr His Met Cys Glu Gln His Ile Asp Arg Lys Cys Pro Asn Cys Gly
 225 230 235 240
 Trp Gly Leu Pro Leu Leu His Met Lys Arg Ala Arg Ile Gln Gln Asn
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 Ser Thr Gly Ser Ser Ser Asn Ala Asp Ile Gln Thr Gln Thr Thr Arg
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 Pro Trp Lys Val Ile Tyr Arg Glu Arg Phe Lys Val Glu Ser Asn Trp
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 Arg Lys Gly His Cys Arg Ile Gln Glu Phe Lys Gly His Met Asp Gly
 290 295 300

Ant.
 Ant.

Val Leu Thr Leu Gln Phe Asn Tyr Arg Leu Leu Phe Thr Gly Ser Tyr
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 Asp Ser Thr Ile Gly Ile Trp Asp Leu Phe Thr Gly Lys Leu Ile Arg
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 Tyr Ile Thr Gly Glu Cys Ile Ser Thr Tyr Arg Gly His Ser Asp Ser
 370 375 380
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 Leu Arg Gly His Thr Glu Trp Val Asn Cys Val Lys Leu His Pro Lys
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 Met Thr Asp Gly Ala Asp Glu Ser Asp Thr Pro Ser Asn Glu Gln Glu
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 Thr Val Leu Asp Glu Asn Ile Pro Tyr Pro Thr His Leu Leu Ser Cys
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 Asp Asn Phe Arg Ile Ile Ser Gly Ser His Asp Gly Ser Ile Lys Val
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 Trp Asp Leu Gln Ser Gly Lys Cys Met His Thr Phe Asn Gly Arg Arg
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 Leu Gln Arg Glu Thr Gln His Thr Gln Thr Gln Ser Leu Gly Asp Lys
 595 600 605

a1
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<210> 9

<211> 2112

<212> DNA

<213> *Saccharomyces cerevisiae*

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<211> 703

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 10

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Ser	Phe	Asp	Pro	Gln	Val	Phe	Pro	Ser	Ser	Leu	Ile	His	Gly	Asp	Asn
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Leu	Leu	Pro	Gln	Asp	Asp	Gln	Ile	Ala	Ser	Asp	Pro	Arg	Ser	Glu	Ser
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Asn	Ser	Cys	Asn	Gly	Asn	Thr	Ser	Ser	Ser	Leu	Pro	Cys	Thr	Asp	Ser
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Tyr	Gln	Tyr	Pro	Leu	Lys	His	Ser	Cys	Thr	Pro	Ser	Phe	Leu	Arg	Lys
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all
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 Gly Ser Gly Thr Ile Gln Ile His Asn Ala Ile Thr Gly Val Leu Glu
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 Ala Arg Leu Glu Gly His Lys Glu Gly Val Trp Ala Val Lys Ile His
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 Glu Asn Thr Leu Val Ser Gly Ser Ile Asp Lys Thr Val Arg Val Trp
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 Asn Ile Glu Lys Ala Lys Cys Thr His Ile Phe Arg Gly His Ile Ser
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 Gly Val Glu Ile Val Glu Pro Asp Gln Pro Tyr Ile Val Ser Gly Ser
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 Arg Asp His Thr Leu Arg Val Trp Lys Leu Pro Lys Asn Thr Asp Pro
 465 470 475 480
 Pro Tyr Leu Pro Asp Asn Thr Asn Ser Ile Asp Arg Trp Glu Lys Asn
 485 490 495
 Pro Tyr Phe Val His Thr Leu Ile Gly His Thr Asp Ser Val Arg Thr
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 Ile Ser Gly Tyr Gly Asp Ile Leu Val Ser Gly Ser Tyr Asp Ser Ser
 515 520 525
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 Gly His Ser Leu Arg Ile Tyr Ser Val Leu Tyr Glu Pro Glu Arg Asn
 545 550 555 560
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 Ser Thr Gly Thr Cys Lys Tyr Val Leu Glu Gly His Asp Ala Phe Val
 580 585 590
 Thr Leu Leu Asn Val Phe Gln Asn Arg Leu Ile Ser Gly Ser Ala Asp
 595 600 605

a!
 ant

Ser Thr Ile Arg Ile Trp Asp Leu Asn Thr Gly Lys Pro Leu Met Val
610 615 620

Leu Pro Ser Asn Ser Gly Tyr Ile Ser Ser Phe Val Ser Asp Glu His
625 630 635 640

Lys Ile Ile Ser Gly Asn Asp Gly Ser Val Lys Leu Trp Asp Val Arg
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Thr Gly Lys Leu Leu Arg Phe Leu Leu Thr Asp Leu Thr Lys Ile Trp
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His Val Asp Phe Asp Ala Met Arg Cys Val Ala Ala Val Gln Arg Asp
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<211> 2175

<212> DNA

<213> Murine sp.

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Al
cont

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 <212> PRT
 <213> Murine sp.

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Ile Ile Pro Glu Lys Asn Ser Leu Arg Gln Thr Tyr Asn Ser Cys Ala
      35          40          45

Arg Leu Cys Ile Asn Gln Glu Thr Val Cys Leu Thr Ser Thr Ala Met
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Lys Thr Glu Asn Cys Val Ala Lys Ala Lys Leu Ala Asn Gly Thr Ser
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Ser Met Ile Val Pro Lys Gln Arg Lys Leu Ser Ala Ser Tyr Glu Lys
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Glu Lys Glu Leu Cys Val Lys Tyr Phe Glu Gln Trp Ser Glu Ser Asp
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Gln Val Glu Phe Val Glu His Leu Ile Ser Gln Met Cys His Tyr Gln
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His Gly His Ile Asn Ser Tyr Leu Lys Pro Met Leu Gln Arg Asp Phe
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Ile Thr Ala Leu Pro Ala Arg Gly Leu Asp His Ile Ala Glu Asn Ile
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Leu Ser Tyr Leu Asp Ala Lys Ser Leu Cys Ala Ala Glu Leu Val Cys
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Lys Glu Trp Tyr Arg Val Thr Ser Asp Gly Met Leu Trp Lys Lys Leu
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Ile Glu Arg Met Val Arg Thr Asp Ser Leu Trp Arg Gly Leu Ala Glu
      195          200          205

Arg Arg Gly Trp Gly Gln Tyr Leu Phe Lys Asn Lys Pro Pro Asp Glu
      210          215          220

Asn Ala Pro Pro Asn Ser Phe Tyr Arg Ala Leu Tyr Pro Lys Ile Ile
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a!
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 485 490 495
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 515 520 525
 Glu Phe Gln Ile Val Ser Ser Ser His Asp Asp Thr Ile Leu Ile Trp
 530 535 540

a!
 amr

Asp Phe Leu Asn Asp Pro Ala Ala His Ala Glu Pro Pro Arg Ser Pro
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Ser Arg Thr Tyr Thr Tyr Ile Ser Arg
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 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: peptide motif

<400> 13
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<210> 14
 <211> 32
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: formula
 sequence

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 <222> (3)...(6)
 <223> any amino acid

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<220>
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<220>
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 <223> aromatic amino acid

A!
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<210> 15
<211> 12
<212> PRT
<213> Unknown Organism
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a' cont

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<223> Description of Unknown Organism: EGF-derived peptide

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<210> 16

<211> 12

<212> PRT

<213> Unknown Organism

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<223> Description of Unknown Organism: EGF-derived peptide

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<210> 17

<211> 32

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: formula sequence

<220>

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<222> (1)

<223> unique amino acid, such as cys or lys

<220>

<221> MOD_RES

<222> (2)...(3)

<223> amino acid residue selected to modulate the affinity of the internalizing peptide for different membranes

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Glu Ala Leu Ala Glu Ala Leu Ala Glu Ala Leu Glu Ala Leu Ala Ala
20 25 30

<210> 18

<211> 8

<212> PRT

<213> Unknown Organism

<220>

Al
any

<223> Description of Unknown Organism: peptide substrate
for N-myristoyl transferase

<400> 18

Gly Asn Ala Ala Ala Arg Arg
1 5

<210> 19

<211> 10

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: peptide derived
from laminin

<400> 19

Cys Asp Pro Gly Tyr Ile Gly Ser Arg Cys
1 5 10

<210> 20

<211> 75

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Nde1-EcoR1 fragment

<400> 20

catatgggtg gctgccgtg cgatatgttc ggttgcggtg ctctccaaa aaagaagaga 60
aaggtagctg gattc 75

<210> 21

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: RGD/SV40 peptide

<400> 21

Met Gly Gly Cys Arg Gly Asp Met Phe Gly Cys Gly Ala Pro Pro Lys
1 5 10 15

Lys Lys Arg Lys Val Ala Gly Phe
20

<210> 22

<211> 225

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Nde1-EcoR1 fragment

a!
ant

<400> 22
 catatggagc cagtagatcc tagactagag ccctggaagc atccaggaag tcagcctaaa 60
 actgcttgta ccaattgcta ttgtaaaaag tggtgctttc attgccaagt ttgtttcata 120
 acaaaagccc ttggcatctc ctatggcagg aagaagcgga gacagcgacg aagacctcct 180
 caaggcagtc agactcatca agtttctcta agtaagcaag gattc 225

<210> 23
 <211> 72
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: engineered HIV-1 tat

<400> 23
 Met Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser
 1 5 10 15
 Gln Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe
 20 25 30
 His Cys Gln Val Cys Phe Ile Thr Lys Ala Leu Gly Ile Ser Tyr Gly
 35 40 45
 Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr
 50 55 60
 His Gln Val Ser Leu Ser Lys Gln
 65 70

<210> 24
 <211> 912
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Nde1-EcoR1 fragment

<400> 24
 catatgacct ctcgccgctc cgtgaagtcg ggtccgcggg aggttccgcg cgatgagtag 60
 gaggatctgt actacacccc gtcttcaggt atggcgagtc ccgatagtcc gcctgacacc 120
 tcccgccgtg gcgcctaca gacacgctcg cgccagaggg gcgaggtccg ttctgctccag 180
 tacgacgagt cggattatgc cctctacggg ggctcgatcat ccgaagacga cgaacacccg 240
 gaggtccccc ggacgcggcg tcccgtttcc ggggcggttt tgtccggccc ggggcctgcg 300
 cgggcgcctc cgccacccgc tgggtccgga ggggcgggac gcacacccac caccgcccc 360
 cgggcccccc gaaccacagc ggtggcgact aaggcccccg cggccccggc ggcggagacc 420
 acccgcggca ggaaatcggc ccagccagaa tccgcgcgac tcccagacgc ccccgcgctc 480
 acggcgccaa cccgatccaa gacacccgcg caggggctgg ccagaaagct gcactttagc 540
 accgcccccc caaaccccgga cgcgcatggt accccccggg tggccggctt taacaagcgc 600
 gtcttctgcg ccgcggtcgg gcgcctggcg gccatgcatg cccggatggc ggcgggtccag 660
 ctctgggaca tgtcgcgtcc gcgcacagac gaagacctca acgaactcct tggcatcacc 720
 accatccgcy tgacggtctg cgagggcaaa aacctgcttc agcgcgccaa cgagttggtg 780
 aatccagacg tgggtgcagga cgtcgacgcy gccacggcga ctcgagggcg ttctgcggcg 840
 tcgcgcccc aagagcgacc tcgagcccca gcccgtccg cttctcgccc cagacggccc 900
 gtcgaggaat tc 912

al
 cont.

<210> 25
 <211> 301
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: engineered HSV-1 VP22

<400> 25

Met Thr Ser Arg Arg Ser Val Lys Ser Gly Pro Arg Glu Val Pro Arg
 1 5 10 15

Asp Glu Tyr Glu Asp Leu Tyr Tyr Thr Pro Ser Ser Gly Met Ala Ser
 20 25 30

Pro Asp Ser Pro Pro Asp Thr Ser Arg Arg Gly Ala Leu Gln Thr Arg
 35 40 45

Ser Arg Gln Arg Gly Glu Val Arg Phe Val Gln Tyr Asp Glu Ser Asp
 50 55 60

Tyr Ala Leu Tyr Gly Gly Ser Ser Ser Glu Asp Asp Glu His Pro Glu
 65 70 75 80

Val Pro Arg Thr Arg Arg Pro Val Ser Gly Ala Val Leu Ser Gly Pro
 85 90 95

Gly Pro Ala Arg Ala Pro Pro Pro Pro Ala Gly Ser Gly Gly Ala Gly
 100 105 110

Arg Thr Pro Thr Thr Ala Pro Arg Ala Pro Arg Thr Gly Arg Val Ala
 115 120 125

Thr Lys Ala Pro Ala Ala Pro Ala Ala Glu Thr Thr Arg Gly Arg Lys
 130 135 140

Ser Ala Gln Pro Glu Ser Ala Ala Leu Pro Asp Ala Pro Ala Ser Thr
 145 150 155 160

Ala Pro Thr Arg Ser Lys Thr Pro Ala Gln Gly Leu Ala Arg Lys Leu
 165 170 175

His Phe Ser Thr Ala Pro Pro Asn Pro Asp Ala Pro Trp Thr Pro Arg
 180 185 190

Val Ala Gly Phe Asn Lys Arg Val Phe Cys Ala Ala Val Gly Arg Leu
 195 200 205

Ala Ala Met His Ala Arg Met Ala Ala Val Gln Leu Trp Asp Met Ser
 210 215 220

Arg Pro Arg Thr Asp Glu Asp Leu Asn Glu Leu Leu Gly Ile Thr Thr
 225 230 235 240

Ile Arg Val Thr Val Cys Glu Gly Lys Asn Leu Leu Gln Arg Ala Asn
 245 250 255

al
 cont

Glu Leu Val Asn Pro Asp Val Val Gln Asp Val Asp Ala Ala Thr Ala
 260 265 270

Thr Arg Gly Arg Ser Ala Ala Ser Arg Pro Thr Glu Arg Pro Arg Ala
 275 280 285

Pro Ala Arg Ser Ala Ser Arg Pro Arg Arg Pro Val Glu
 290 295 300

<210> 26

<211> 120

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: NdeI-EcoRI fragment

<400> 26

catatggacg tcgacgcggc cacggcgact cgagggcggt ctgcggcgtc gcgccccacc 60
 gagcgacctc gagccccagc ccgctccgct tctcgcccca gacggcccgt cgaggaattc 120

<210> 27

<211> 37

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: VP22 (C-terminal domain)

<400> 27

Met Asp Val Asp Ala Ala Thr Ala Thr Arg Gly Arg Ser Ala Ala Ser
 1 5 10 15

Arg Pro Thr Glu Arg Pro Arg Ala Pro Ala Arg Ser Ala Ser Arg Pro
 20 25 30

Arg Arg Pro Val Glu
 35

<210> 28

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic or
 natural linker

<400> 28

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
 1 5 10 15

ant

<210> 29
 <211> 4
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: tetrapeptide
 isostere

<400> 29
 Ala Ile Tyr Tyr
 1

<210> 30
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 30
 gcggatccac catggataam aaagaggac ctaataac 38

<210> 31
 <211> 76
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 31
 gcgcggccgc ctactcatca tcactagatg gcamcttctg agcaaaacag ccctctggta 60
 ttatagttgt cctcgt 76

<210> 32
 <211> 72
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 32
 cgcgccgcc tactcatcat cactagatgg camttgagcc aaagttttct ctggtattat 60
 agttgtcctc gt 72

<210> 33
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>

21
 cont

<221> modified_base
 <222> (20)
 <223> i

<220>
 <223> Description of Artificial Sequence: primer

<400> 33
 gcwatccacc atggataatn taaagaggga cctaataac 39

<210> 34
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 34
 gtaggtgtat ctccatgtgg tatratagtr gtcc 34

<210> 35
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 35
 ggacaactat aataccacat ggagatacac ctac 34

<210> 36
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 36
 gcctcgagtc actcctcctc tgagctgtc 29

<210> 37
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 37
 gcggatccac catggataam aaagaggac ctaataac 38

a!
 Cont

<210> 38
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 38
 cctatcacat ctatatttta ttggtattat agttgtc

37

<210> 39
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 39
 gacaactata ataccaataa aatatagatg tgatagg

37

<210> 40
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 40
 gcctcgagtc ataatgtgtt agtatattgt cctg

34

<210> 41
 <211> 69
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 41
 gcggatccac catggaggaa gaagagtata tgcccatgga ggagactctt tgccaacggt 60
 ttaaattgtg 69

<210> 42
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

a!
 cont

<400> 42
gcgcggccgc tcatatagac ataatccag tagac 35

<210> 43
<211> 65
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 43
gcggatccgc caccatggac tacaaggacg acgatgacaa agatgacccg gccgaggcgg 60
tgctg 65

<210> 44
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 44
gtaggtgtat ctccatgtct ggagatgtag gtgtatg 37

<210> 45
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 45
catacaccta catctccaga catggagata cacctac 37

<210> 46
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 46
gcgcggccgc tcactcctcc tctgagctgt c 31

<210> 47
<211> 5
<212> PRT
<213> Unknown Organism

al
cont

a¹
ant

<220>

<223> Description of Unknown Organism: LFCSE motif

<400> 47

Leu Phe Cys Ser Glu

1

5
